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B2



#8

SEQUENCE LISTING

<110> Lyamichev, Victor
Skrzypczynski, Zbigniew
Allawi, Hatim T.
Wayland, Sarah R.
Takova, Tsetska
Neir, Bruce P.

<120> Charge Tags and the Separation of Nucleic Acid Molecules

<130> FORS-04912

<140> 09/777,430

<141> 2001-02-06

<160> 85

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caccac 2526

<210> 15

<211> 842

<212> PRT

<213> *Thermus thermophilus*

<400> 15

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 16

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16
gcctgcaggg gcggccgcgt gcaccggggc a

31

<210> 17

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17
ctcctggacc cttcgaacac cacccc

26

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 18
 gtcctggccc atatggaggc cac 23
 <210> 19
 <211> 2526
 <212> DNA
 <213> *Thermus thermophilus*
 <400> 19
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 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccc acccccaggg acttcccccg gcagctcgcc 300
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 ggcacgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
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 gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
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 gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgaccc catgctcctc 1140

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cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accgggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	acccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgctt	ggggaagacg	caaaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctcc	caagcctcgt	ccaccgagg	1680
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gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
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gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggtca	ccaccaccac	2520
caccac						2526

<210> 20

<211> 842

<212> PRT

<213> *Thermus thermophilus*

<400> 20

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 21

caggaggagc tcgttgccga cctggaggag

30

<210> 22

<211> 2526

<212> DNA

<213> Thermus thermophilus

<400> 22

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60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccgggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg cagtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc

240

tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc

300

ctcatcaagg agctggtgga cctcctggggg ttaccgccg tgcaggtccc cggctacgag

360

gaggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420
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acgggcccgc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
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 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaaggggtca ccaccaccac 2520
 caccac 2526

<210> 23

<211> 842

<212> PRT

<213> *Thermus thermophilus*

<400> 23

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 24

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 24
ggagcgttg cctgtcttct tcgtcttctt caaggcggga ggcct 45

<210> 25

<211> 2526

<212> DNA

<213> *Thermus thermophilus*

<400> 25
atgaattccg aggcgatgct tccgtctttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttccg ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccagag acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgca cctctaccaa ctgctctccg accgcgtcgc cgtcctccac 480
cccaggggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccagaccg gaggggctta gggccttcct ggagaggctg 840
gagttcgga gcctcctcca cgagttcggc ctctggagg cccccgccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctccc ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca 1020
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttggt cctcgaggga ggggctagac ctggtgccc gggacgacct catgctcctc 1140
gcctacctcc tggacccttc gaacaccacc cccgaggggg tggcgcgcg ctacgggggg 1200
gagtggacgg aggacgccc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc 1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac 1500

gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccctacg ggaggccac cccatcgtagg agaagatcct ccagcaccgg 1620
gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
acggggccgcc tccacacccg cttcaaccag acggccacgg ccacgggggag gcttagtagc 1740
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gccttcgtgg ccgaggcggg ttgggcgttg gtggcccttg actatagcca gatagagctc 1860
cgcgctcctg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
gacatccaca cccagaccgc aagctggatg ttcggcgctcc ccccgagggc cgtggacccc 1980
ctgatgcgcc gggcggccaa gacggtgaac ttcggcgctcc tctacggcat gtccgcccat 2040
aggtctctcc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100
ttccaaagct tccccaaggt gcgggccttg atagaaaaga ccctggagga ggggaggaag 2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacac caacgcccgg 2220
gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccgt ccagggcacc 2280
gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
gcccgcacgc tctccaggt cgccaacgag ctctccttg agggccccca agcgcgggccc 2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460
ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 26

<211> 842

<212> PRT

<213> *Thermus thermophilus*

<400> 26

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
245 250 255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
260 265 270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
275 280 285
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
290 295 300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 27

<211> 340

<212> PRT

<213> Pyrococcus furiosus

<400> 27

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
1 5 10 15

Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
20 25 30

Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
35 40 45

Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
50 55 60

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175

 Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190

 Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205

 Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220

 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240

 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255

 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270

 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285

 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300

 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320

 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335

 Trp Phe Lys Arg
 340

<210> 28

<211> 326

<212> PRT

<213> Methanococcus jannaschii

<400> 28

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
85 90 95

Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
100 105 110

Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
130 135 140

Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160

Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
165 170 175

Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
180 185 190

Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
195 200 205

Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
210 215 220

Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
225 230 235 240

Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
260 265 270

Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
305 310 315 320

Leu Asp Ala Trp Phe Lys
325

<210> 29

<211> 328

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 29

Met Gly Val Lys Leu Arg Asp Val Val Ser Pro Arg Arg Ile Arg Leu
1 5 10 15

Glu Asp Leu Arg Gly Arg Thr Val Ala Val Asp Ala Ala Asn Thr Leu
20 25 30

Tyr Gln Phe Leu Ser Ser Ile Arg Gln Arg Asp Gly Thr Pro Leu Met
35 40 45

Asp Ser Arg Gly Arg Val Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Thr Ala Ala Val Met Glu Arg Glu Ile Arg Val Ile Tyr Val Phe Asp
65 70 75 80

Gly Arg Ser His His Leu Lys Gly Glu Thr Val Ser Arg Arg Ala Asp
85 90 95

Ile Arg Lys Lys Ser Glu Val Glu Trp Lys Arg Ala Leu Glu Glu Gly
100 105 110

Asp Ile Asp Arg Ala Arg Lys Tyr Ala Val Arg Ser Ser Arg Met Ser
115 120 125

Ser Glu Ile Leu Glu Ser Ser Lys Arg Leu Leu Glu Leu Leu Gly Ile
130 135 140

Pro Tyr Val Gln Ala Pro Gly Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160

Val Lys Met Gly Asp Ala Trp Ala Val Ala Ser Gln Asp Tyr Asp Cys
165 170 175

Leu Leu Phe Gly Ala Pro Arg Val Val Arg Lys Val Thr Leu Ser Gly
180 185 190

Lys Leu Glu Asp Pro His Ile Ile Glu Leu Glu Ser Thr Leu Arg Ala
195 200 205

Leu Ser Ile Ser His Thr Gln Leu Val Asp Met Ala Leu Leu Val Gly
210 215 220

Thr Asp Phe Asn Glu Gly Val Lys Gly Tyr Gly Ala Arg Arg Gly Leu
225 230 235 240

Lys Leu Ile Arg Glu Lys Gly Asp Ile Phe Lys Val Ile Arg Asp Leu
245 250 255

Glu Ala Asp Ile Gly Gly Asp Pro Gln Val Leu Arg Arg Ile Phe Leu
260 265 270

Glu Pro Glu Val Ser Glu Asp Tyr Glu Ile Arg Trp Arg Lys Pro Asp
275 280 285

Val Glu Gly Val Ile Glu Phe Leu Cys Thr Glu His Gly Phe Ser Glu
290 295 300

Asp Arg Val Arg Asp Ala Leu Lys Lys Phe Glu Gly Ala Ser Ser Thr
305 310 315 320

Gln Lys Ser Leu Glu Asp Trp Phe
325

<210> 30

<211> 336

<212> PRT

<213> Archaeoglobus fulgidus

<400> 30

Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1 5 10 15

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (18)..(18)

<223> The n at this position can be a, c, t, or g.

<220>

<221> misc_feature

<222> (27)..(27)

<223> The n at this position can be a, c, t, or g.

<400> 31

atctctagca ctgctgtntt ygayggn

27

<210> 32
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The n at this position can be a, c, t, or g.
 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The n at this position can be a, c, t, or g.
 <400> 32
 gatctctagc actgctgarg gngargcnca r 31
 <210> 33
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 33
 gatctctagc actgctcarg aytaygay 28
 <210> 34
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature

<222> (20)..(20)
 <223> The n at this position can be a, c, t, or g.
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The n at this position can be a, c, t, or g.
 <400> 34
 cttaaggtag gactacytgn gcytcnccyt c 31
 <210> 35
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 35
 ttaaggtagg actacytcrt aytcytgrct 30
 <210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The n at this position can be a, c, t, or g.
 <400> 36
 ttaaggtagg actacytcrt aytcytgnga 30

<210> 37
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (25)..(25)
 <223> The n at this position can be a, c, t, or g.
 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The n at this position can be a, c, t, or g.
 <400> 37
 ttaaggtagg actacrtrw artcngtncc 30
 <210> 38
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 38
 gatctctagc actgct 16
 <210> 39
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 39
 ccttaaggta ggactac 17

<210> 40
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 40
 tatcgacgcg atccacttct cctctgc 27
 <210> 41
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 41
 cttaaacggc aacctgagaa ggcttgg 27
 <210> 42
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 42
 ctatctcctt ctgcttgaaa acaggagg 28
 <210> 43
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 43
 acaaggaac agctcgatga tatcgcg 27

<210> 44
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 44
 taacgaattc ggtgcagaca taggcgaact ac 32
 <210> 45
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 45
 cgggtgtcgac tcaggaaaac cacctctcaa gcg 33
 <210> 46
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 46
 cacaggaaac agaccatggg tgcagacata ggcgaac 37
 <210> 47
 <211> 1017
 <212> DNA
 <213> Archaeoglobus veneficus
 <400> 47
 atgggtgcag acataggcga actactcgag agagaagaag ttgaacttga gtacttctcc 60
 gggagaaaaa tagctattga tgcttttaac actctttacc agttcatatc tatcataagg 120
 caacctgacg gcactccttt gaaggattct cagggtagaa tgacctcaca cctctccggc 180
 atcctgtacc gcgtgtcaaa catgatcgag gttggaatga gacccatttt cgtttttcgat 240

ggtgagcctc ctgttttcaa gcagaaggag atagaggaac gaaaggaaaag aagagctgaa 300
 gcagaggaga agtggatcgc tgcgatagag agaggagaga agtacgcaaa gaagtacgct 360
 caggcagcgg cgaggggttga tgaatacatc gtcgagtcgt caaagaagct gcttgagtat 420
 atgggagttc catgggttca ggcgccgagt gagggagagg cacaggctgc atacatggca 480
 gcgaagggcg atgtagattt tactggctcg caggattacg actcgcttct cttcggcagc 540
 ccaaagcttg caagaaatct cgcgattact ggaaagagga agctgcccgg aaagaatggt 600
 tacgttgagg tcaaaccaga gataatagac ttaaacggca acctgagaag gcttgggaata 660
 acaagggaaac agctcgtcga tatcgcgttg ctcgtgggaa cggactacaa cgaaggagtg 720
 aagggcgttg ggggtcaagaa ggcctacaag tacataaaaa cctacggaga tgttttcaaa 780
 gctctcaagg ccttaaaggt agagcaggag aacatagagg agataagaaa cttcttcctg 840
 aacccgcctg ttacgaacaa ctacagcctc cacttcggaa agccagacga tgagaagatt 900
 atcgagttcc tgtgtgaaga gcacgacttt agcaaggata gggtagagaa ggccgttgag 960
 aagctgaaaag caggaatgca agcctcgcaa tcaacgcttg agaggtgggtt ttcctga 1017

<210> 48

<211> 338

<212> PRT

<213> Archaeoglobus veneficus

<400> 48

Met Gly Ala Asp Ile Gly Glu Leu Leu Glu Arg Glu Glu Val Glu Leu
 1 5 10 15

Glu Tyr Phe Ser Gly Arg Lys Ile Ala Ile Asp Ala Phe Asn Thr Leu
 20 25 30

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45

Asp Ser Gln Gly Arg Met Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60

Val Ser Asn Met Ile Glu Val Gly Met Arg Pro Ile Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Val Phe Lys Gln Lys Glu Ile Glu Glu Arg Lys Glu
 85 90 95

Arg Arg Ala Glu Ala Glu Glu Lys Trp Ile Ala Ala Ile Glu Arg Gly
 100 105 110

Glu Lys Tyr Ala Lys Lys Tyr Ala Gln Ala Ala Ala Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Glu Ser Ser Lys Lys Leu Leu Glu Tyr Met Gly Val Pro
 130 135 140
 Trp Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Asp Phe Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Lys Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Val Lys Pro Glu Ile
 195 200 205
 Ile Asp Leu Asn Gly Asn Leu Arg Arg Leu Gly Ile Thr Arg Glu Gln
 210 215 220
 Leu Val Asp Ile Ala Leu Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Tyr Lys Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Val Phe Lys Ala Leu Lys Ala Leu Lys Val Glu Gln Glu Asn Ile
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asn Asn Tyr
 275 280 285
 Ser Leu His Phe Gly Lys Pro Asp Asp Glu Lys Ile Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Lys Asp Arg Val Glu Lys Ala Val Glu
 305 310 315 320
 Lys Leu Lys Ala Gly Met Gln Ala Ser Gln Ser Thr Leu Glu Arg Trp
 325 330 335
 Phe Ser

<210> 49
 <211> 53
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 49
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53
 <210> 50
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing either a Cy3 or fluorescein group.
 <220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The T residues at these positions have amino-modifiers.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The residue at this position is linked to a spacer containing either a Cy3 or fluorescein group.
 <400> 50
 ttccagagcc taatttgcca gt 22

<210> 51
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing either a Cy3 or fluorescein group.
 <220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The T residues at these positions have amino-modifiers.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The residue at this position is linked to a spacer containing either a Cy3 or fluorescein group.

 <400> 51
 ttccagagcc taatttgcca gt 22

 <210> 52
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing either a TET or fluorescein group.

<400> 52	
ttccagagcc taatttgcca gta	23
<210> 53	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<220>	
<221> misc_feature	
<222> (1)..(1)	
<223> The residue at this position is linked to a spacer containing either a TET or fluorescein group.	
<400> 53	
ttccagagcc taatttgcca gta	23
<210> 54	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 54	
cttaccaacg ctaacgagcg tcttg	25
<210> 55	
<211> 14	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic	
<400> 55	
gctcccgcag acac	14

<210> 56
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a C
 y3 group.
 <220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The residues at these positions have amino modifications.
 <400> 56
 ttacgccacc agct 14
 <210> 57
 <211> 12
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 57
 cgctgtctcg ct 12
 <210> 58
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 58
 gctcaaggca ctcttgccc 19

<210> 59
 <211> 63
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 59
 atgactgaat ataaacttgt ggtagttgga gctggtggcg taggcaagag tgccttgacg 60
 ata 63
 <210> 60
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 60
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgt 45
 <210> 61
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 61
 cttcggagtt tggg 14
 <210> 62
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 62
 cttcggagtt tggg 14

<210>	63	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	63	
	cttcggagtt tggg	14
<210>	64	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	64	
	cttcggagtt tggg	14
<210>	65	
<211>	14	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	65	
	cttcggagtt tggg	14
<210>	66	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic	
<400>	66	
	gggttggtga gtgagtgttc aagta	25

<210> 67
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 67
 ccatacctaatac gactcact atagggc 27
 <210> 68
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 68
 ctcatacagttacttgtcttc 21
 <210> 69
 <211> 489
 <212> RNA
 <213> Homo sapiens
 <400> 69
 gaacucacua uagggcucga gcggccgccc gggcaggucc gccacaaaaa ugcagauuuu 60
 cgugaaaacc cuuacgggga agaccaucac ccucgagguu gaacccucgg auacgauaga 120
 aaauuaaag gccaaagaucc aggaauagga aggaauuccu ccugaucagc agagacugau 180
 cuuugcuggc aagcagcugg aagauggacg uacuuugucu gacuacaaua uucaaaagga 240
 gucuacucuu caucuugugu ugagacuucg ugguggugcu aagaaaagga agaagaaguc 300
 uuacaccacu cccaagaaga auaagcaca gagaaagaag guuaagcugg cuguccugaa 360
 auauuaaag guggaugaga auggcaaaa uagucgccuu cgucgagagu gcccuucuga 420
 ugaauuggu gcuggggugu uuauggcaag ucacuuugac agacauuuu guggcaaaug 480
 uugucugac 489

<210> 70
 <211> 52
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 70
 ggaatacgcac tcactatagg gaaagtctct gccgcccttc tgtgcctgct gc 52
 <210> 71
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 71
 aatagttaca aaatattcat ttccacaata a 31
 <210> 72
 <211> 647
 <212> RNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 72
 gggaaagucu cugccgcccu ucugugccug cugcucauag cagccaccuu cauuccccaa 60
 gggcucgcuc agccagaugc aaucaaugcc ccagucaccu gcuguuauaa cuucaccaau 120
 aggaagaucu cagugcagag gcucgcgagc uauagaagaa ucaccagcag caaguguccc 180
 aaagaagcug ugaucuucaa gaccuuugug gccaaaggaga ucugugcuga cccaagcag 240
 aaguggguuc aggauuccau ggaccaccug gacaagcaaa cccaaacucc gaagacuuga 300
 acacucacuc cacaacccaa gaucugcag cuaacuuauu uuccccuagc uuuccccaga 360
 caccucguuu uauuuuuaua uaaugaauuu uguuuguuga ugugaaacau uaugccuuaa 420
 guaauguuaa uucuuuuua aguuuuugau guuuuaaguu uaucuuuau gguacuagug 480

uuuuuuagau acagagacuu ggggaaauug cuuuuccucu ugaaccacag uucuaccccu 540
gggauguuuu gagggucuuu gcaagaauc auaauacaaa gaauuuuuuu uaacauucca 600
augcauugcu aaaauauuau uguggaaaug aaauuuuugu aacuaau 647
<210> 73
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 73
ttcttcggag tttggg 16
<210> 74
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 74
ccgtcacgcc tccttcggag tttggg 26
<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 75
aacccaaact ccgaaggagg cgtg 24
<210> 76
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 76
 gcgcagtgag aatgaggagg cgtgacggt 29
 <210> 77
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a C
 y3 group.
 <400> 77
 ctcattctca gtgcg 15
 <210> 78
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 78
 aacgaggcgc acctttacat tttctatcgt 30
 <210> 79
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 79
 ccttccttat cctggatcct ggca 24

<210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 80
 acgataaaaa atgtaaagggt gcgc 24
 <210> 81
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 81
 cggaagaagc aagtgggtgcg cctcggttaa 29
 <210> 82
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a C
 y3 group.
 <400> 82
 cacttgettc ctcc 14

<210> 83
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 83
 gctcccgcag acac 14
 <210> 84
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 84
 caaagaaaag ctgcgtgatg atgaaatcgc 30
 <210> 85
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 85
 gaagggtgtct gcgggagccg atttcatcat cacgcagctt ttctttgagg 50

~~61~~ 154